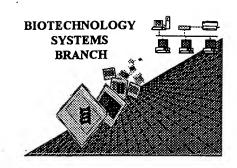
RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

er: <u>09/451,739</u>

Art Unit / Team No.:

BARA 1643 3-24

Date Processed by STIC:

4/13/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

BATCH (1643) (3-24)

PAGE: 1

RAW SEQUENCE LISTING

PATENT APPLICATION US/09/451,739

DATE: 04/13/2000 TIME: 13:46:18

Input Set: I451739.RAW

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

```
<110> Jager, Dirk
           Scanlan, Matthew
                                                       Does Not Comply
           Gure, Ali
           Jager, Elke
                                                   Corrected Diskette Needed
           Knuth, Alexander
           Old, Lloyd
 6
           Chen, Yao-tseng
     <120> Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigens,
 8
           the Antigens per se, and Uses Thereof
 9
10
    <130> LUD 5615
    <140> US/09/451,739
11
     <141> 1999-11-30
12
     <160> 19
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ERORED SEQUENCES FOLLOW

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     <2116 528
15
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16
17
     <213> Homo sapiens
     <220>
18
19
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20
21
22
           Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala
23
           Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn
24
25
           Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln
26
27
           Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr
28
29
                               70
                                                    75
           Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu
30
31
                                                90
32
           Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly
33
34
           Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys Ala
35
                                        120
36
           Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys
37
                                    135
                                                        140
38
           Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn
39
           145
                               150
                                                    155
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PAGE:

2

RAW SEQUENCE LISTING

DATE: 04/13/2000 TIME: 13:46:18

PATENT APPLICATION US/09/451,739

Input Set: I451739.RAW

Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met 11 165 170 175 22 Phe Pro Ser Glu Ser Lys Gln Lys Lys Val Glu Glu Asn Ser Trp Asp 130 180 190 24 Ser Glu Ser Leu Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro 25 200 205 26 Lys Ala Thr His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu 210 225 230 235 240 25 Arg Ala Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys 25 Lys Leu Glu His Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys 26 Glu Ala Lys Glu Heu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys 27 278 260 27 278 260 Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp 290 Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp 290 Glu Ala Lys Glu Glu Gln His Arg Lys Glu Leu Glu Val Lys Glu Glu 305 Gly Arg Ile Glu Gln His Arg Lys Glu Leu Glu Val Lys Glu Glu 310 315 320 Lys Arg Arg Asn Ala Asp Ile Leu Asn Gln Lys Val Lys Trp 290 Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln 340 62 Leu Glu Gln Ala Leu Arg Ile Gln Asp Ile Glu Lys Ser Val Glu 315 326 63 315 64 Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Gln Asn Tyr Leu 385 64 Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu 390 66 Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu 390 67 385 68 Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr 405 406 69 Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met 427 428 429 429 425 430 425 430 445 446 457 467 467 468 470 475 480 481 481 481 485 490 490 495 490 495 490 496 490 497 485 490 490 490 491 491 491 491 491														_				
Phe Pro Ser Glu Ser Lys Gln Lys Lys Val Glu Glu Asn Ser Trp Asp 180 180 180 180 185 180 185 180 200 205 205 206 207 207 208 208 208 208 209 208 209 209 209 209 209 209 209 209 209 209	40	Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Gln	Met	
180	41					165					170					175		
Ser Glu Ser Leu Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro	42	Phe	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Lys	Val	Glu	Glu	Asn	Ser	Trp	Asp	
195	43				180		_		_	185					190	_	_	
195	44	Ser	Glu	Ser	Leu	Arq	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Val	Pro	
Lys Ala Thr His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu 210 215 Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu 225 Arg Ala Arg Alu Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys 225 Met Glu Gln Met Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser 230 Arg Ala Arg Alu Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys 225 Met Glu Gln Met Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser 230 235 Met Glu Gln Met Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser 230 230 Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp 230 230 Glu Glu Leu Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Glu 330 330 330 330 330 331 330 330 331 330 331 330 331 330 331 345 350 Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln 345 356 361 362 Leu Glu Gln Ala Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Glu 335 360 370 375 380 681 Glu Ha Ala Thr Leu Lys His Thr His Glu Asn Glu Asn Tyr Leu 385 390 682 Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr 400 401 402 425 430 431 432 440 445 440 445 440 451 465 Asp Leu Lys Glu Lys Glu Asn Thr Met Leu Gln Met 457 468 Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser 450 460 470 480 481 482 483 484 485 486 Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp 500 82 Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile						•						•			4			
48		Lvs	Ala		His	Gln	Lvs	Glu		Asp	Lvs	Ile	Ser		Lvs	Leu	Glu	
Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu 225 226 227 230 Arg Ala Arg Glu Leu Ghn Lys Asp His Cys Glu Gln Arg Thr Gly Lys 51 Wet Glu Gln Met Lys Lys Lys Fhe Cys Val Leu Lys Lys Lys Lys Leu Ser 237 240 258 Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp 290 295 300 Glu Gln Glu Leu Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Glu 305 Glu Gln Glu Leu Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Glu 305 Gly Arg Arg Asn Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu 325 Gly Arg Ile Glu Gln His Arg Lys Glu Leu Glu Val Lys Ser Val Glu 340 355 Gly Arg Ile Glu Gln His Arg Lys Glu Leu Glu Val Lys Ser Val Glu 355 Gly Arg Ile Glu Gln His Arg Lys Glu Leu Lys Ser Val Glu 355 Gly Arg Ile Glu Ser His Thr His Glu Asn Glu Asn Tyr Leu 370 385 Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu 370 385 Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr 405 Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr 405 Thr Leu Lys Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr 435 A45 A45 A45 A45 A45 A45 A46 Ser Gly Gln Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr 465 A70 A75 A76 Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser 450 A45 A45 A45 A45 A45 A46 Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile 467 A67 A68 Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile A167 A17 A65 Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile A470 A45 A45 A46 A470 A470 A471 A465 A470 A472 A473 A475 A480 A474 A475 A480 A475 A480 A481 A481 A481 A481 A481 A481 A481 A481		-1-					-4				_1 _			1				
Arg Ala Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys Fig. 1 260 / 250 / 2		Asp		Thr	Ser	Leu	Ser		Ile	Leu	Asp	Thr	_	His	Ser	Cvs	Glu	
Arg Ala Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys	•	_														-1-		
Met Glu Gln Met Lys Lys Phe Cys Val Leu Lys Lys Leu Ser 270	J/V J		Ala	Ara	Glu	Leu		Lvs	Asp	His	Cvs		Gln	Ara	Thr	Glv	,	Λα
Met Glu Gln Met Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser 280 280 280 280 280 280 280 280 280 280								-1					<u> </u>					please
275 260 280 265 285 276 285	אנו נונו	Met	Glu	•		, ,		Lvs	•		,		Lvs	•				
Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp 290 300 300 310 310 315 320 320 321 325 320 325 326 327 328 328 329 329 320 325 320 325 320 325 320 325 326 327 327 328 329 329 320 325 320 325 320 325 320 326 327 327 328 329 320 321 320 320 321 320 320 321 320 320 320 320 320 320 320 320 320 320	Clar.					-1-	-7-	-1,-				-,		. –	~~~			align
295 300 295 300 320 325 320 320 335 320	K9/1	Glu				Tle	Lvs	Ser				Asn				Lvs	Tro	,
Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu 370 375 380 66				-1-			-1-							-1-		-1-		amoralia
Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu 370 375 380 66	r	Glu		Glu	Leu	Cvs	Ser		Arσ	Len	Thr	Len		Gln	Glu	Glu	Glu	humbers
Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu 370 375 380 66	1		0111	O_u		0,0			9					0.11	<u></u>	014		14 16
Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu 370 375 380 66			Δrσ	Δrα	Δgn	Δla		Tle	T. 0 11	Δαn	Glu		Tle	Δra	Glu	Glu		wan
Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu 370 375 380 66		_,,	9	9								_,_		9			204	then.
Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu 370 375 380 66		Glv	Δrσ	Tle	Glu		Gln	His	Δrσ	Lvs		T.e.ii	Glu	Val	Lvs		Gln	water
Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu 370 375 380 66		1	9						5	_					_			respect
Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu 370 375 380 66		Leu	Glu	Gln		Leu	Ara	Ile	Gln		Ile	Glu	Leu	Lvs		Val	Glu	anero \
65							3							_				audi)
65	64	Ser	Asn	Leu	Asn	Gln	Val	Ser	His	Thr	His	Glu	Asn	Glu	Asn	Tyr	Leu	
67	65		370					375					380					•
68 Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr 69	66	Leu	His	Glu	Asn	Cys	Met	Leu	Lys	Lys	Glu	Ile	Ala	Met	Leu	Lys	Leu	
69 Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met 71 420 72 Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr 73 435 74 Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser 75 450 76 Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu 77 465 78 Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile 79 79 70 70 71 71 72 73 74 75 76 77 78 78 78 78 78 79 78 79 79 79 79 70 70 71 71 71 72 73 74 75 76 77 78 78 78 78 78 78 78 78 78 78 78 78	67	385					390					395					400	
70 Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met 71 420 425 430 72 Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr 73 435 440 445 74 Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser 75 450 455 460 76 Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu 77 465 470 475 480 78 Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile 495 80 Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp 81 500 505 510 82 Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile	68	Glu	Ile	Ala	Thr	Leu	Lys	His	Gln	Tyr	Gln	Glu	Lys	Glu	Asn	Lys	Tyr	
71	69					405					410					415		
Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr 73	70	Phe	Glu	Asp	Ile	Lys	Ile	Leu	Lys	Glu	Lys	Asn	Ala	Glu	Leu	${\tt Gln}$	Met	
73	71				420					425					430			
74 Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser 75 450 455 460 76 Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu 460 77 465 470 475 480 78 Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile 490 495 80 Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp 495 81 500 505 510 82 Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile	72	Thr	Leu	Lys	Leu	Lys	Glu	Glu	Ser	Leu	Thr	Lys	Arg	Ala	Ser	Gln	Tyr	
75	73			435					440					445				
76 Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu 77 465 470 475 480 78 Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile 490 495 80 Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp 500 505 510 82 Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile	74	Ser	Gly	Gln	Leu	Lys	Val	Leu	Ile	Ala	Glu	Asn	Thr	Met	Leu	Thr	Ser	
77 465 470 475 480 78 Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile 79 485 490 495 80 Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp 81 500 505 510 82 Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile	75		450					455					460					
Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile 485 490 495 Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp 500 505 510 Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile	76	Lys	Leu	Lys	Glu	Lys	Gln	Asp	Lys	Glu	Ile	Leu	Glu	Ala	Glu	Ile	Glu	
79 485 490 495 80 Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp 81 500 505 510 82 Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile	77	465					470					475					480	
80 Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp 81 500 505 510 82 Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile	78	Ser	His	His	Pro	Arg	Leu	Ala	Ser	Ala	Val	Gln	Asp	His	Asp	Gln	Ile	
81 500 505 510 82 Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile	79					485					490					495		
82 Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile	80	Val	Thr	Ser	Arg	Lys	Ser	Gln	Glu	Pro	Ala	Phe	His	Ile	Ala	Gly	Asp	
	81				500					505					510			
83 515 520 525	82	Ala	Cys	Leu	Gln	Arg	Lys	Met	Asn	Val	Asp	Val	Ser	Ser	Thr	Asp	Ile	
	83			515					520					525				
	 								_		-							

E--> 84 <210> 19 294(sext page)

^{86 &}lt;212> PRT

^{87 &}lt;213> Homo sapiens

^{88 &}lt;220>

PAGE :

RAW SEQUENCE LISTING

DATE: 04/13/2000 TIME: 13:46:18

PATENT APPLICATION US/09/451,739

Input Set: I451739.RAW

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92		Asp	Pro	Gly	Pro	Val	Ala	Arg	Gly	Arg	Gly	Cys	Ser	Ser	Asp	Arg	Leu
93					20					25					30		
94		Pro	Arg	Pro	Ala	Gly	Pro	Ala	Arg	Arg	Gln	Phe	${\tt Gln}$	Ala	Ala	Ser	Leu
95				35					40					45			
96		Leu	Thr	Arg	Gly	Trp	Gly	Arg	Ala	Trp	${\tt Pro}$	${\tt Trp}$	Lys	${\tt Gln}$	Ile	Leu	Lys
97			50					55					60				
98		Glu	Leu	Asp	Glu	Cys	Tyr	Glu	Arg	Phe	Ser	Arg	Glu	Thr	Asp	Gly	Ala
99		65					70					75					80
100		Gln	Lys	Arg	Arg	Met	Leu	His	Cys	Val	Gln	Arg	Ala	Leu	Ile	Arg	Ser
101						85					90					95	
102		Gln	Glu	Leu	Gly	Asp	Glu	Lys	Ile	${\tt Gln}$	Ile	Val	Ser	${\tt Gln}$	Met	Val	Glu
103					1,00					105					110		
104		Leu	Val	Glu	Asn	Arg	Thr	Arg	Gln	Val	Asp	Ser	His	Val	Glu	Leu	Phe
105				115					120					125			
106		Glu	Ala	Gln	Gln	Glu	Leu	Gly	Asp	Thr	Val	Gly	Asn	Ser	Gly	Lys	Val
107			130					135					140				
108		Gly	Ala	Asp	Arg	Pro	Asn	Gly	Asp	Ala	Val	Ala	${\tt Gln}$	Ser	Asp	Lys	Pro
109		145					150					155					160
110		Asn	Ser	Lys	Arg	Ser	Arg	Arg	Gln	Arg	Asn	Asn	Glu	Asn	Arg	Glu	Asn
111						165					170					175	
112		Ala	Ser	Ser	Asn	His	Asp	His	Asp	Asp	Gly	Ala	Ser	Gly	Thr	Pro	Lys
113					180					185					190		
114		Glu	Lys	Lys	Ala	Lys	Thr	Ser	Lys	Lys	Lys	Lys	Arg	Ser	Lys	Ala	Lys
115				195					200					205			
116		Ala	Glu	Arg	Glu	Ala	Ser	Pro	Ala	Asp	Leu	Pro	Ile	Asp	Pro	Asn	Glu
117			210					215					220				
118	, i	Pro	Thr	Tyr	Cys	Leu	Cys	Asn	Gln	Val	Ser	Tyr	Gly	Glu	Met	Ile	Gly
119	Jun	225					230					235					240
120	my,	Cys	Asp				Cys	Pro	Ile				His	Phe			Val
121	Th -					245					250					255	
122	M,	Gly	Leu			Lys	Pro	Lys			Trp	Tyr	Cys	Pro	Lys	Cys	Arg
123	ì		_	275			_		280	•	_				270		
124	1	Gly			Glu	Lys	Thr			ГÀ	Ala				Ser	Lys	Lys
125		_	29 0					295	780				300	285			
126	<u>.</u>		Arg	Ala	Tyr	Asn								_			
127		305	240				3 10 -	•					1	1			

Please review the

Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

PAGE:

VERIFICATION SUMMARY
PATENT APPLICATION US/09/451,739

DATE: 04/13/2000

TIME: 13:46:18

Input Set: I451739.RAW

Line ? Error/Warning Original Text

15 E Input 528, Calc Seq.Length 512 differ <211> 528

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